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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/099,619

DATE: 04/03/2002

TIME: 14:51:40

Input Set : A:\2001.001US.txt

Output Set: N:\CRF3\04032002\J099619.raw

3 <110> APPLICANT: CLAESSENS, JOHANNES AJ
4 WALTER, FUCHS
6 <120> TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS VACCINE
8 <130> FILE REFERENCE: 2001001US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/099,619
11 <141> CURRENT FILING DATE: 2002-03-15
13 <150> PRIOR APPLICATION NUMBER: EP012009759
14 <151> PRIOR FILING DATE: 2001-03-15
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1711
22 <212> TYPE: DNA
23 <213> ORGANISM: AVIAN INFLUENZA VIRUS
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (11)..(1705)
28 <223> OTHER INFORMATION: ISOLATE A/ITALY/445/99 (H7/N1)
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33 Met Asn Thr Gln Ile Leu Val Phe Ala Leu Val Ala Ile
34 1 5 10
36 att ccg aca agt gca gac aaa atc tgc ctt ggg cat cat gcc gtg tca 97
37 Ile Pro Thr Ser Ala Asp Lys Ile Cys Leu Gly His His Ala Val Ser
38 15 20 25
40 aac ggg act aaa gta aac aca tta act gaa aga gga gtg gaa gtc gtt 145
41 Asn Gly Thr Lys Val Asn Thr Leu Thr Glu Arg Gly Val Glu Val Val
42 30 35 40 45
44 aat gca act gaa acg gtg gaa cga aca aac gtc ccc agg atc tgc tca 193
45 Asn Ala Thr Glu Thr Val Glu Arg Thr Asn Val Pro Arg Ile Cys Ser
46 50 55 60
48 aaa ggg aaa agg aca gtt gac ctc ggt caa tgt gga ctt ctg gga aca 241
49 Lys Gly Lys Arg Thr Val Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr
50 65 70 75
52 atc act ggg cca ccc caa tgt gac cag ttc cta gaa ttt tca gcc gat 289
53 Ile Thr Gly Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Ser Ala Asp
54 80 85 90
56 cta att att gag agg cga gaa gga agt gat gtc tgt tat cct ggg aaa 337
57 Leu Ile Ile Glu Arg Arg Glu Gly Ser Asp Val Cys Tyr Pro Gly Lys
58 95 100 105
60 ttc gtg aat gaa gaa gct ctg agg caa att ctc agg gag tca ggc gga 385
61 Phe Val Asn Glu Glu Ala Leu Arg Gln Ile Leu Arg Glu Ser Gly Gly
62 110 115 120 125

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TECH CENTER 1600/2300

64	att gac aag gag gca atg gga ttc aca tac agc gga ata aga act aat	433
65	Ile Asp Lys Glu Ala Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn	
66	130 135 140	
68	gga aca acc agt aca tgt agg aga tca gga tct tca ttc tat gca gag	481
69	Gly Thr Thr Ser Thr Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu	
70	145 150 155	
72	atg aaa tgg ctc ctg tca aac aca gac aat gct gct ttc ccg cag atg	529
73	Met Lys Trp Leu Leu Ser Asn Thr Asp Asn Ala Ala Phe Pro Gln Met	
74	160 165 170	
76	act aag tca tac aaa aac aca agg aaa gac cca gct ctg ata ata tgg	577
77	Thr Lys Ser Tyr Lys Asn Thr Arg Lys Asp Pro Ala Leu Ile Ile Trp	
78	175 180 185	
80	ggg atc cac cat tcc gga tca act aca gaa cag acc aag cta tat ggg	625
81	Gly Ile His His Ser Gly Ser Thr Thr Glu Gln Thr Lys Leu Tyr Gly	
82	190 195 200 205	
84	agt gga aac aaa ctg ata aca gtt ggg agt tct aat tac caa cag tcc	673
85	Ser Gly Asn Lys Leu Ile Thr Val Gly Ser Ser Asn Tyr Gln Gln Ser	
86	210 215 220	
88	ttt gta ccg agt cca gga gag aga cca caa gtg aat ggc caa tct gga	721
89	Phe Val Pro Ser Pro Gly Glu Arg Pro Gln Val Asn Gly Gln Ser Gly	
90	225 230 235	
92	aga att gac ttt cat tgg ctg atg cta aac ccc aat gac aca gtc act	769
93	Arg Ile Asp Phe His Trp Leu Met Leu Asn Pro Asn Asp Thr Val Thr	
94	240 245 250	
96	ttc agt ttc aat ggg gcc ttc ata gct cca gac cgt gca agt ttt ctg	817
97	Phe Ser Phe Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Ser Phe Leu	
98	255 260 265	
100	aga ggg aag tct atg ggg att cag agt gga gta cag gtt gat gcc aat	865
101	Arg Gly Lys Ser Met Gly Ile Gln Ser Gly Val Gln Val Asp Ala Asn	
102	270 275 280 285	
104	tgt gaa gga gat tgc tat cac agt gga ggg aca ata ata agt aat ttg	913
105	Cys Glu Gly Asp Cys Tyr His Ser Gly Gly Thr Ile Ile Ser Asn Leu	
106	290 295 300	
108	ccc ttt cag aac ata aat agc agg gca gta ggg aaa tgt ccg aga tat	961
109	Pro Phe Gln Asn Ile Asn Ser Arg Ala Val Gly Lys Cys Pro Arg Tyr	
110	305 310 315	
112	gtt aag caa gag agt ctg ctg ctg gca aca ggg atg aag aat gtt ccc	1009
113	Val Lys Gln Glu Ser Leu Leu Leu Ala Thr Gly Met Lys Asn Val Pro	
114	320 325 330	
116	gaa att cca aaa gga tcg cgt gtg agg aga ggc cta ttt ggt gct ata	1057
117	Glu Ile Pro Lys Gly Ser Arg Val Arg Arg Gly Leu Phe Gly Ala Ile	
118	335 340 345	
120	gcg ggt ttc att gaa aat gga tgg gaa ggt ctg att gat ggg tgg tat	1105
121	Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly Leu Ile Asp Gly Trp Tyr	
122	350 355 360 365	
124	ggc ttc agg cat caa aat gca caa gga gag gga act gct gca gat tac	1153
125	Gly Phe Arg His Gln Asn Ala Gln Gly Glu Gly Thr Ala Ala Asp Tyr	
126	370 375 380	
128	aaa agc acc caa tca gca att gat caa gta aca gga aaa ttg aac ccg	1201

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129 Lys Ser Thr Gln Ser Ala Ile Asp Gln Val Thr Gly Lys Leu Asn Arg
130      385      390      395
132 ctt ata gaa aaa act aac caa caa ttt gag tta ata gac aat gaa ttc      1249
133 Leu Ile Glu Lys Thr Asn Gln Gln Phe Glu Leu Ile Asp Asn Glu Phe
134      400      405      410
136 act gag gtt gaa aag caa att ggc aat gtg ata aat tgg acc aga gat      1297
137 Thr Glu Val Glu Lys Gln Ile Gly Asn Val Ile Asn Trp Thr Arg Asp
138      415      420      425
140 tcc atg aca gaa gtg tgg tcc tat aac gct gaa ctc ttg gta gca atg      1345
141 Ser Met Thr Glu Val Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Met
142 430      435      440      445
144 gag aac cag cat aca att gat ctg acc gac tca gaa atg aac aaa cta      1393
145 Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu Met Asn Lys Leu
146      450      455      460
148 tac gaa cga gtg aag aga cta ctg aga gag aat gct gaa gaa gat ggc      1441
149 Tyr Glu Arg Val Lys Arg Leu Leu Arg Glu Asn Ala Glu Glu Asp Gly
150      465      470      475
152 act ggt tgc ttc gaa ata ttt cac aag tgt gat gac gat tgt atg gcc      1489
153 Thr Gly Cys Phe Glu Ile Phe His Lys Cys Asp Asp Cys Met Ala
154      480      485      490
156 agt att aga aac aac aca tat gat cac agc aag tac agg gaa gag gca      1537
157 Ser Ile Arg Asn Asn Thr Tyr Asp His Ser Lys Tyr Arg Glu Glu Ala
158      495      500      505
160 atg caa aat aga ata cag att gac cca gtc aaa cta agc agc ggc tac      1585
161 Met Gln Asn Arg Ile Gln Ile Asp Pro Val Lys Leu Ser Ser Gly Tyr
162 510      515      520      525
164 aaa gat gtg ata ctt tgg ttt agc ttc ggg gca tca tgt ttc ata ctt      1633
165 Lys Asp Val Ile Leu Trp Phe Ser Phe Gly Ala Ser Cys Phe Ile Leu
166      530      535      540
168 ctg gcc att gca atg ggc ctt gtc ttc ata tgt gtg aga aat gga aac      1681
169 Leu Ala Ile Ala Met Gly Leu Val Phe Ile Cys Val Arg Asn Gly Asn
170      545      550      555
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173 Met Arg Cys Thr Ile Cys Ile
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177 <210> SEQ ID NO: 2
178 <211> LENGTH: 564
179 <212> TYPE: PRT
180 <213> ORGANISM: AVIAN INFLUENZA VIRUS
182 <400> SEQUENCE: 2
184 Met Asn Thr Gln Ile Leu Val Phe Ala Leu Val Ala Ile Ile Pro Thr
185 1      5      10      15
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189      20      25      30
192 Lys Val Asn Thr Leu Thr Glu Arg Gly Val Glu Val Val Asn Ala Thr
193      35      40      45
196 Glu Thr Val Glu Arg Thr Asn Val Pro Arg Ile Cys Ser Lys Gly Lys
197      50      55      60
200 Arg Thr Val Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr Ile Thr Gly

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201 65              70              75              80
204 Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Ser Ala Asp Leu Ile Ile
205              85              90              95
208 Glu Arg Arg Glu Gly Ser Asp Val Cys Tyr Pro Gly Lys Phe Val Asn
209              100              105              110
212 Glu Glu Ala Leu Arg Gln Ile Leu Arg Glu Ser Gly Gly Ile Asp Lys
213              115              120              125
216 Glu Ala Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn Gly Thr Thr
217              130              135              140
220 Ser Thr Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu Met Lys Trp
221 145              150              155              160
224 Leu Leu Ser Asn Thr Asp Asn Ala Ala Phe Pro Gln Met Thr Lys Ser
225              165              170              175
228 Tyr Lys Asn Thr Arg Lys Asp Pro Ala Leu Ile Ile Trp Gly Ile His
229              180              185              190
232 His Ser Gly Ser Thr Thr Glu Gln Thr Lys Leu Tyr Gly Ser Gly Asn
233              195              200              205
236 Lys Leu Ile Thr Val Gly Ser Ser Asn Tyr Gln Gln Ser Phe Val Pro
237              210              215              220
240 Ser Pro Gly Glu Arg Pro Gln Val Asn Gly Gln Ser Gly Arg Ile Asp
241 225              230              235              240
244 Phe His Trp Leu Met Leu Asn Pro Asn Asp Thr Val Thr Phe Ser Phe
245              245              250              255
248 Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Ser Phe Leu Arg Gly Lys
249              260              265              270
252 Ser Met Gly Ile Gln Ser Gly Val Gln Val Asp Ala Asn Cys Glu Gly
253              275              280              285
256 Asp Cys Tyr His Ser Gly Gly Thr Ile Ile Ser Asn Leu Pro Phe Gln
257              290              295              300
260 Asn Ile Asn Ser Arg Ala Val Gly Lys Cys Pro Arg Tyr Val Lys Gln
261 305              310              315              320
264 Glu Ser Leu Leu Leu Ala Thr Gly Met Lys Asn Val Pro Glu Ile Pro
265              325              330              335
268 Lys Gly Ser Arg Val Arg Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe
269              340              345              350
272 Ile Glu Asn Gly Trp Glu Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg
273              355              360              365
276 His Gln Asn Ala Gln Gly Glu Gly Thr Ala Ala Asp Tyr Lys Ser Thr
277              370              375              380
280 Gln Ser Ala Ile Asp Gln Val Thr Gly Lys Leu Asn Arg Leu Ile Glu
281 385              390              395              400
284 Lys Thr Asn Gln Gln Phe Glu Leu Ile Asp Asn Glu Phe Thr Glu Val
285              405              410              415
288 Glu Lys Gln Ile Gly Asn Val Ile Asn Trp Thr Arg Asp Ser Met Thr
289              420              425              430
292 Glu Val Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Met Glu Asn Gln
293              435              440              445
296 His Thr Ile Asp Leu Thr Asp Ser Glu Met Asn Lys Leu Tyr Glu Arg
297              450              455              460

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300 Val Lys Arg Leu Leu Arg Glu Asn Ala Glu Glu Asp Gly Thr Gly Cys
301 465                               470                               475                               480
304 Phe Glu Ile Phe His Lys Cys Asp Asp Asp Cys Met Ala Ser Ile Arg
305                               485                               490                               495
308 Asn Asn Thr Tyr Asp His Ser Lys Tyr Arg Glu Glu Ala Met Gln Asn
309                               500                               505                               510
312 Arg Ile Gln Ile Asp Pro Val Lys Leu Ser Ser Gly Tyr Lys Asp Val
313                               515                               520                               525
316 Ile Leu Trp Phe Ser Phe Gly Ala Ser Cys Phe Ile Leu Leu Ala Ile
317                               530                               535                               540
320 Ala Met Gly Leu Val Phe Ile Cys Val Arg Asn Gly Asn Met Arg Cys
321 545                               550                               555                               560
324 Thr Ile Cys Ile

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/099,619

DATE: 04/03/2002

TIME: 14:51:42

Input Set : A:\2001.001US.txt

Output Set: N:\CRF3\04032002\J099619.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number